

BLAST comparison of coding sequence for attractin (5' untranslated region and 3' untranslated region removed).

Reference sequence: human membrane attractin (long 5' end)

Identity to itself:

Homo sapiens attractin (ATRN), transcript variant 1, mRNA, Length = 8645

Score = 8504 bits (4290), Expect = 0.0

Identities = 4290/4290 (100%)

Strand = Plus / Plus

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Query: 1      atggtggctgcagcggcggaactgaggcaaggctgaggaggaggacggcgggcgacggca 60
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Sbjct: 80      atggtggctgcagcggcggaactgaggcaaggctgaggaggaggacggcgggcgacggca 139

Query: 61      gcgctcgcgggcaggagcggcgggccgcactgggactgggacgtgaccagggctgggagg 120
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Sbjct: 140     gcgctcgcgggcaggagcggcgggccgcactgggactgggacgtgaccagggctgggagg 199

Query: 121     ccggggctgggggcccgggctgcgcctcccgcggctgctgtctccaccgctgcggccacgg 180
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Sbjct: 200     ccggggctgggggcccgggctgcgcctcccgcggctgctgtctccaccgctgcggccacgg 259

Query: 181     ctgctgctgctgctgttggtgctctcgccgcgctgctgctgctgctgctgacctgtgag 240
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Sbjct: 260     ctgctgctgctgctgttggtgctctcgccgcgctgctgctgctgctgctgacctgtgag 319

Query: 241     gccgaggccgcggcgggcgggcgggcggtgtcgggctcagccgcagccgaggccaaggaa 300
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Sbjct: 320     gccgaggccgcggcgggcgggcgggcggtgtcgggctcagccgcagccgaggccaaggaa 379

Query: 301     tgtgaccggccctgtgtcaacggcggtcgctgcaaccctggcaccggccagtgcgtctgc 360
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Sbjct: 380     tgtgaccggccctgtgtcaacggcggtcgctgcaaccctggcaccggccagtgcgtctgc 439

Query: 361     cccgccggctgggtgggagcaatgccagcactgcgggggcccgttcagactaactgga 420
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Sbjct: 440     cccgccggctgggtgggagcaatgccagcactgcgggggcccgttcagactaactgga 499

Query: 421     tcttctgggtttgtgacagatggacctggaaattataaatacaaaacgaagtgcacgtgg 480
             |||
Sbjct: 500     tcttctgggtttgtgacagatggacctggaaattataaatacaaaacgaagtgcacgtgg 559

Query: 481     ct cattgaaggacagccaaatagaataatgagacttcgtttcaatcattttgctacagag 540
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Sbjct: 560 ctcattgaaggacagccaaatagaataatgagacttcgtttcaatcattttgctacagag 619

Query: 541 tgtagttgggaccattttatatgtttatgatggggactcaattttatgcaccgctagttgct 600
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 Sbjct: 620 tgtagttgggaccattttatatgtttatgatggggactcaattttatgcaccgctagttgct 679

Query: 601 gcatttagtggcctcattgttcctgagagagatggcaatgagactgtccctgaggttggt 660
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 Sbjct: 680 gcatttagtggcctcattgttcctgagagagatggcaatgagactgtccctgaggttggt 739

Query: 661 gccacatcagggttatgccttgctgcatttttttagtgatgctgcttataatttgactgga 720
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 Sbjct: 740 gccacatcagggttatgccttgctgcatttttttagtgatgctgcttataatttgactgga 799

Query: 721 tttaatattacttacagttttgatatgtgtccaaataactgctcaggccgaggagagtggt 780
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 Sbjct: 800 tttaatattacttacagttttgatatgtgtccaaataactgctcaggccgaggagagtggt 859

Query: 781 aagatcagtaatagcagcgatactgttgaatgtgaatgttctgaaaactggaaaggtgaa 840
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 Sbjct: 860 aagatcagtaatagcagcgatactgttgaatgtgaatgttctgaaaactggaaaggtgaa 919

Query: 841 gcatgtgacattcctcactgtacagacaactgtgggttttcctcatcgaggcatctgcaat 900
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 Sbjct: 920 gcatgtgacattcctcactgtacagacaactgtgggttttcctcatcgaggcatctgcaat 979

Query: 901 tcaagtgatgtcagaggatgctcctgcttctcagactggcagggctcctggatgttcagtt 960
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 Sbjct: 980 tcaagtgatgtcagaggatgctcctgcttctcagactggcagggctcctggatgttcagtt 1039

Query: 961 cctgtaccagctaaccagtcattttggactcgagaggaatattctaacttaaagctcccc 1020
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 Sbjct: 1040 cctgtaccagctaaccagtcattttggactcgagaggaatattctaacttaaagctcccc 1099

Query: 1021 agagcatctcataaaagctgtgggtcaatggaaacattatgtggggtgttgaggatatatg 1080
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 Sbjct: 1100 agagcatctcataaaagctgtgggtcaatggaaacattatgtggggtgttgaggatatatg 1159

Query: 1081 ttcaaccactcagattataacatggttctagcgtatgaccttgcttctagggagtggctt 1140
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 Sbjct: 1160 ttcaaccactcagattataacatggttctagcgtatgaccttgcttctagggagtggctt 1219

Query: 1141 ccactaaaccgttctgtgaacaatgtgggttgttagatatgggtcattccttggcattatac 1200
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 Sbjct: 1220 ccactaaaccgttctgtgaacaatgtgggttgttagatatgggtcattccttggcattatac 1279

Query: 1201 aaggataaaatttacatgtatggaggaaaaattgattcaactgggaatgtgaccaatgag 1260
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 Sbjct: 1280 aaggataaaatttacatgtatggaggaaaaattgattcaactgggaatgtgaccaatgag 1339

Query: 1261 ttgagagtttttcacattcataatgagtcattgggtggttgaccctaaggcaaaggag 1320
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 Sbjct: 1340 ttgagagtttttcacattcataatgagtcattgggtggttgaccctaaggcaaaggag 1399

Query: 1321 cagtatgcagtgggtgggcactctgcacacattgttacactgaagaatggccgagtgggc 1380
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 Sbjct: 1400 cagtatgcagtgggtgggcactctgcacacattgttacactgaagaatggccgagtgggc 1459

Query: 1381 atgctgggtcatctttgggtcactgccctctctatggatatataagcaatgtgcaggaatat 1440
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 Sbjct: 1460 atgctgggtcatctttgggtcactgccctctctatggatatataagcaatgtgcaggaatat 1519

Query: 1441 gatttggataagaacacatggagtatattacacacccagggtgcccttgtgcaaggggggt 1500
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 Sbjct: 1520 gatttggataagaacacatggagtatattacacacccagggtgcccttgtgcaaggggggt 1579

Query: 1501 tacggccatagcagtgtttacgaccataggaccaggggccctatacgttcatgggtggctac 1560
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 Sbjct: 1580 tacggccatagcagtgtttacgaccataggaccaggggccctatacgttcatgggtggctac 1639

Query: 1561 aaggctttcagtgccataaagtaccggcttgcagatgatctctaccgatatgatgtggat 1620
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 Sbjct: 1640 aaggctttcagtgccataaagtaccggcttgcagatgatctctaccgatatgatgtggat 1699

Query: 1621 acccagatgtggaccattcttaaggacagccgatttttccggttacttgacacagctgtg 1680
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 Sbjct: 1700 acccagatgtggaccattcttaaggacagccgatttttccggttacttgacacagctgtg 1759

Query: 1681 atagtgagtggaaccatgctggtgtttggaggaaacacacacaatgacacatctatgagc 1740
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 Sbjct: 1760 atagtgagtggaaccatgctggtgtttggaggaaacacacacaatgacacatctatgagc 1819

Query: 1741 catggcgccaaatgcttctcttcagatttcatggcctatgacattgctgtgaccgctgg 1800
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Query: 1861 ttacacaacagcaccatgtatgtgttcggtggtttcaatagtctcctcctcagcgacatc 1920

Sbjct: 1940 |||||
 ttacacaacagcaccatgtatgtgttcggtggtttcaatagtctcctcctcagcgacatc 1999

Query: 1921 ctggtattcacctcggaacagtgtgatgcgcacatcgagtggaagccgcttgtagcagca 1980
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Sbjct: 2000 ctggtattcacctcggaacagtgtgatgcgcacatcgagtggaagccgcttgtagcagca 2059

Query: 1981 ggacctggtattcggtgtgtgtggaacacagggctcgtctcagtgtatctcgtgggcgctg 2040
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Sbjct: 2060 ggacctggtattcggtgtgtgtggaacacagggctcgtctcagtgtatctcgtgggcgctg 2119

Query: 2041 gcaactgatgaacaagaagaaaagttaaaatcagaatgtttttccaaaagaactcttgac 2100
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Sbjct: 2120 gcaactgatgaacaagaagaaaagttaaaatcagaatgtttttccaaaagaactcttgac 2179

Query: 2101 catgacagatgtgaccagcacacagattgttacagctgcacagccaacaccaatgactgc 2160
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Sbjct: 2180 catgacagatgtgaccagcacacagattgttacagctgcacagccaacaccaatgactgc 2239

Query: 2161 cactggtgcaatgaccattgtgtccccaggaaccacagctgctcagaaggccagatctcc 2220
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Sbjct: 2240 cactggtgcaatgaccattgtgtccccaggaaccacagctgctcagaaggccagatctcc 2299

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Sbjct: 2300 attttttaggtatgagaattgccccaggataacccccatgtactactgtaacaagaagacc 2359

Query: 2281 agctgcaggagctgtgccctggaccagaactgccagtgaggagccccggaatcaggagtg 2340
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Sbjct: 2360 agctgcaggagctgtgccctggaccagaactgccagtgaggagccccggaatcaggagtg 2419

Query: 2341 attgccctgcccgaataatctgtggcattggctggcatttggttggaactcatgtttg 2400
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Query: 2401 aaaattactactgccaaggagaattatgacaatgctaaattgttctgtaggaaccacaat 2460
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Sbjct: 2480 aaaattactactgccaaggagaattatgacaatgctaaattgttctgtaggaaccacaat 2539

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Query: 2521 ataatgcagtcactctcagagcatgtccaagctcaccttaaccccatgggtcggccttcgg 2580
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Query: 2641 cagtggatgccgtctgagcccagtgatgctggattctgtggaattttatcagaacccagt 2700
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Query: 2761 cctgcaaaccacagtgctaagcagtgccggacaccatgtgccttgaggacagcatgtgga 2820
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Query: 2821 gattgcaccagcggcagctctgagtgcattgtggtgcagcaacatgaagcagtggtggac 2880
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Query: 2881 tccaatgcctatgtggcctccttcccttttgccagtgatatggaatggtatacgatgagc 2940
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Query: 2941 acctgccccctgaaaattgttcaggctactgtacctgtagtcattgcttgaggcaacca 3000
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 Sbjct: 3080 ggctgtggctggtgtactgatcccagcaatactggcaaagggaaatgcatagagggttcc 3139

Query: 3061 tataaaggaccagtgaagatgccttcgcaagccccctacaggaaatttctatccacagccc 3120
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 Sbjct: 3140 tataaaggaccagtgaagatgccttcgcaagccccctacaggaaatttctatccacagccc 3199

Query: 3121 ctgctcaattccagcatgtgtctagaggacagcagatacaactggctctttcattcactgt 3180
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 Sbjct: 3200 ctgctcaattccagcatgtgtctagaggacagcagatacaactggctctttcattcactgt 3259

Query: 3181 ccagcttgccaatgcaacggccacagtaaatgcatcaatcagagcatctgtgagaagtgt 3240
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 Sbjct: 3260 ccagcttgccaatgcaacggccacagtaaatgcatcaatcagagcatctgtgagaagtgt 3319

Query: 3241 gagaacctgaccacaggcaagcactgcgagacctgcataatctggcttctacgggtgatccc 3300
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 Sbjct: 3320 gagaacctgaccacaggcaagcactgcgagacctgcataatctggcttctacgggtgatccc 3379

Query: 3301 accaatggaggggaaatgtcagccatgcaagtgcaatgggcacgcgtctctgtgcaacacc 3360
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 Sbjct: 3380 accaatggaggggaaatgtcagccatgcaagtgcaatgggcacgcgtctctgtgcaacacc 3439

Query: 3361 aacacgggcaagtgcttctgcaccaccaagggcgtaagggggacgagtgccagctatgt 3420
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 Sbjct: 3440 aacacgggcaagtgcttctgcaccaccaagggcgtaagggggacgagtgccagctatgt 3499

Query: 3421 gaggtagaaaaatcgataccaaggaaaccctctcagaggaacatgttattatactcttctt 3480
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 Sbjct: 3500 gaggtagaaaaatcgataccaaggaaaccctctcagaggaacatgttattatactcttctt 3559

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Query: 3541 aattttgtggctactcctgacgaacaaaacagggatttggacatgttcatcaatgcctcc 3600
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Query: 3661 gaagagatgcctgttgtttcaaaaaccaacattaaggagtacaaagatagtttctctaatt 3720
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Query: 3721 gagaagtttgattttcgcaaccacccaaatatcactttctttgtttatgtcagtaatttc 3780
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Query: 3781 acctggcccatcaaaaattcagattgccttctctcagcacagcaattttatggacctggta 3840
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Query: 3841 cagttcttcgtgactttcttcagttgtttcctctctttgctcctgggtggctgctgtggtt 3900
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Sbjct: 3980 tggaagatcaaacaagttgttgggcctccagacgtagagagcaacttcttcgagagatg 4039

Query: 3961 caacagatggccagccgtccctttgcctctgtaaatgtcgcccttggaacagatgaggag 4020
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Sbjct: 4040 caacagatggccagccgtccctttgcctctgtaaatgtcgcccttggaacagatgaggag 4099

Query: 4021 cctcctgatcttattggggggagtataaagactgttcccaaaccattgcactggagccg 4080
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Sbjct: 4100 cctcctgatcttattggggggagtataaagactgttcccaaaccattgcactggagccg 4159

Query: 4081 tgttttggcaacaaagccgctgtcctctctgtgtttgtgaggctccctcgaggcctgggt 4140
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Sbjct: 4160 tgttttggcaacaaagccgctgtcctctctgtgtttgtgaggctccctcgaggcctgggt 4219

Query: 4141 ggcatccctcctcctgggcagtcaggtcttgcctgtggccagcgccctgggtggacatttct 4200
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Sbjct: 4220 ggcatccctcctcctgggcagtcaggtcttgcctgtggccagcgccctgggtggacatttct 4279

Query: 4201 cagcagatgccgatagtgtacaaggagaagtcaggagccgtgagaaaccggaagcagcag 4260
|||||

Sbjct: 4280 cagcagatgccgatagtgtacaaggagaagtcaggagccgtgagaaaccggaagcagcag 4339

Query: 4261 cccctgcacagcctgggacctgcatctga 4290
|||||

Sbjct: 4340 cccctgcacagcctgggacctgcatctga 4369

Identity to secreted attractin (long 5' end)

Homo sapiens attractin (ATRN), transcript variant 2, mRNA, Length = 4116

Score = 7535 bits (3801), Expect = 0.0

Identities = 3801/3801 (100%)

Strand = Plus / Plus

100% identical base pairs, but 88.6% of length therefore 88.6% identical (?)

Query: 1 atggtggctgcagcggcggaactgaggcaaggctgaggaggaggacggcgggcgacggca 60
|||||

Sbjct: 80 atggtggctgcagcggcggaactgaggcaaggctgaggaggaggacggcgggcgacggca 139

Query: 61 gcgctcgcgggcaggagcggcgggccgcactgggactgggacgtgaccagggctgggagg 120
|||||

Sbjct: 140 gcgctcgcgggcaggagcggcgggccgcactgggactgggacgtgaccagggctgggagg 199

Query: 121 ccggggctgggggcccgggctgcgcctcccgcggctgctgtctccaccgctgcggccacgg 180
|||||

Sbjct: 200 ccggggctgggggcccgggctgcgcctcccgcggctgctgtctccaccgctgcggccacgg 259

Query: 181 ctgctgctgctgctgttggtgctctcgccgcccgtgctgctgctgctgctgcccctgtgag 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 260 ctgctgctgctgctgttggtgctctcgccgcccgtgctgctgctgctgctgcccctgtgag 319

Query: 241 gccgaggccgcggcggcgggcgggcggtgtcgggctcagccgcagccgaggccaaggaa 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 320 gccgaggccgcggcggcgggcgggcggtgtcgggctcagccgcagccgaggccaaggaa 379

Query: 301 tgtgaccggccctgtgtcaacggcggtcgctgcaaccctggcaccggccagtgcgtctgc 360
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 Sbjct: 380 tgtgaccggccctgtgtcaacggcggtcgctgcaaccctggcaccggccagtgcgtctgc 439

Query: 361 cccgccggctgggtgggcgagcaatgccagcactgcgggggcccgttcagactaactgga 420
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 Sbjct: 440 cccgccggctgggtgggcgagcaatgccagcactgcgggggcccgttcagactaactgga 499

Query: 421 tcttctgggtttgtgacagatggacctggaaattataaatacaaaaacgaagtgcacgtgg 480
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 500 tcttctgggtttgtgacagatggacctggaaattataaatacaaaaacgaagtgcacgtgg 559

Query: 481 ctcattgaaggacagccaaatagaataatgagacttcgtttcaatcattttgctacagag 540
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 Sbjct: 560 ctcattgaaggacagccaaatagaataatgagacttcgtttcaatcattttgctacagag 619

Query: 541 tgtagttgggaccatttatatgtttatgatggggactcaatttatgcaccgctagtgtgct 600
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Query: 601 gcatttagtggcctcattgttcctgagagagatggcaatgagactgtccctgaggttgtt 660
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Query: 3781 acctggcccatcaaaattcag 3801
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 Sbjct: 3860 acctggcccatcaaaattcag 3880

Identity to secreted attractin (short 5' end)

Homo sapiens attractin (ATRN), transcript variant 3, mRNA, Length = 3894

Score = 6918 bits (3490), Expect = 0.0
 Identities = 3490/3490 (100%)
 Strand = Plus / Plus

100% identical base pairs over first 92 base pairs, then deleted region, then 100% identical over 3490 base pairs; therefore 100% identical over 92+3490 bp = 3582 bp, therefore 83.5% of reference length therefore 83.5% identical (?)

Query: 312 ctgtgtcaacggcggtcgctgcaaccctggcaccggccagtgcgctgccccgccggctg 371
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Query: 1992 tcggtgtgtgtggaacacagggctcgtctcagtgtatctcgtggcgctggcaactgatga 2051
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 Sbjct: 1849 tcggtgtgtgtggaacacagggctcgtctcagtgtatctcgtggcgctggcaactgatga 1908

Query: 2052 acaagaagaaaagttaaaatcagaatgtttttccaaaagaactcttgaccatgacagatg 2111
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 1909 acaagaagaaaagttaaaatcagaatgtttttccaaaagaactcttgaccatgacagatg 1968

Query: 2112 tgaccagcacacagattgttacagctgcacagccaacaccaatgactgccactggtgcaa 2171
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 1969 tgaccagcacacagattgttacagctgcacagccaacaccaatgactgccactggtgcaa 2028

Query: 2172 tgaccattgtgtccccaggaaccacagctgctcagaaggccagatctccatttttaggta 2231
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 2029 tgaccattgtgtccccaggaaccacagctgctcagaaggccagatctccatttttaggta 2088

Query: 2232 tgagaattgccccaaaggataaccccatgtactactgtaacaagaagaccagctgcaggag 2291
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 Sbjct: 2089 tgagaattgccccaaaggataaccccatgtactactgtaacaagaagaccagctgcaggag 2148

Query: 2292 ctgtgccctggaccagaactgccagtgggagccccggaatcaggagtgcattgccctgcc 2351
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 2149 ctgtgccctggaccagaactgccagtgggagccccggaatcaggagtgcattgccctgcc 2208

Query: 2352 cgaaaaatatctgtggcattggctggcatttggttggaactcatgtttgaaaattactac 2411
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 Sbjct: 2209 cgaaaaatatctgtggcattggctggcatttggttggaactcatgtttgaaaattactac 2268

Query: 2412 tgccaaggagaattatgacaatgctaaattgttctgtaggaaccacaatgcccttttggc 2471
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 Sbjct: 2269 tgccaaggagaattatgacaatgctaaattgttctgtaggaaccacaatgcccttttggc 2328

Query: 2472 ttctcttacaaccacagaagaaggtagaatttgtccttaagcagctgccaataatgcagtc 2531
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 Sbjct: 2329 ttctcttacaaccacagaagaaggtagaatttgtccttaagcagctgccaataatgcagtc 2388

Query: 2532 atctcagagcatgtccaagctcaccttaaccccatgggtcggccttcggaagatcaatgt 2591
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 2389 atctcagagcatgtccaagctcaccttaaccccatgggtcggccttcggaagatcaatgt 2448

Query: 2592 gtcctactggtgctgggaagatatgtccccatttacaaatagtttactacagtggatgcc 2651
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Sbjct: 2449 gtctactggtgctgggaagatatgtccccatttacaaatagtttactacagtggatgcc 2508

Query: 2652 gtctgagcccagtgatgctggattctgtggaatTTTatcagaaccagTactcggggact 2711
|||||

Sbjct: 2509 gtctgagcccagtgatgctggattctgtggaatTTTatcagaaccagTactcggggact 2568

Query: 2712 gaaggctgcaacctgcatcaaccactcaatggtagtgctgtgaaaggcctgcaaacca 2771
|||||

Sbjct: 2569 gaaggctgcaacctgcatcaaccactcaatggtagtgctgtgaaaggcctgcaaacca 2628

Query: 2772 cagtgcctaagcagtgccggacaccatgtgccttgaggacagcatgtggagattgcaccag 2831
|||||

Sbjct: 2629 cagtgcctaagcagtgccggacaccatgtgccttgaggacagcatgtggagattgcaccag 2688

Query: 2832 cggcagctctgagtgcattggtgcagcaacatgaagcagtggtggactccaatgccta 2891
|||||

Sbjct: 2689 cggcagctctgagtgcattggtgcagcaacatgaagcagtggtggactccaatgccta 2748

Query: 2892 tgtggcctccttccctTTTtgccagtgatggaatggTatacgatgagcacctgcccccc 2951
|||||

Sbjct: 2749 tgtggcctccttccctTTTtgccagtgatggaatggTatacgatgagcacctgcccccc 2808

Query: 2952 tgaaaattgttcaggctactgtacctgtagtcattgcttgagcaaccaggctgtggctg 3011
|||||

Sbjct: 2809 tgaaaattgttcaggctactgtacctgtagtcattgcttgagcaaccaggctgtggctg 2868

Query: 3012 gtgtactgatcccagcaataactggcaaagggaatgcatagagggttcctataaaggacc 3071
|||||

Sbjct: 2869 gtgtactgatcccagcaataactggcaaagggaatgcatagagggttcctataaaggacc 2928

Query: 3072 agtgaagatgccttcgcaagcccctacaggaaatttctatccacagcccctgctcaattc 3131
|||||

Sbjct: 2929 agtgaagatgccttcgcaagcccctacaggaaatttctatccacagcccctgctcaattc 2988

Query: 3132 cagcatgtgtctagaggacagcagatacaactggcttttcattcactgtccagcttgcca 3191
|||||

Sbjct: 2989 cagcatgtgtctagaggacagcagatacaactggcttttcattcactgtccagcttgcca 3048

Query: 3192 atgcaacggccacagtaaTgcatcaatcagagcatctgtgagaagtgtgagaacctgac 3251
|||||

Sbjct: 3049 atgcaacggccacagtaaTgcatcaatcagagcatctgtgagaagtgtgagaacctgac 3108

Query: 3252 cacaggcaagcactgcgagacctgcatatctggcttctacggtgatcccacaaTggagg 3311
|||||

Sbjct: 3109 cacaggcaagcactgcgagacctgcatatctggcttctacggtgatcccacaaTggagg 3168

Query: 3312 gaaatgtcagccatgcaagtgcaatgggcacgcgtctctgtgcaacaccaacacgggcaa 3371
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 3169 gaaatgtcagccatgcaagtgcaatgggcacgcgtctctgtgcaacaccaacacgggcaa 3228

Query: 3372 gtgcttctgcaccaccaagggcggtcaagggggacgagtgccagctatgtgaggtagaaaa 3431
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 3229 gtgcttctgcaccaccaagggcggtcaagggggacgagtgccagctatgtgaggtagaaaa 3288

Query: 3432 tcgataccaaggaaaccctctcagaggaacatggtattataactcttcttattgactatca 3491
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 3289 tcgataccaaggaaaccctctcagaggaacatggtattataactcttcttattgactatca 3348

Query: 3492 gttcaccttttagtctatcccaggaagatgatcgctattacacagctatcaattttgaggc 3551
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 3349 gttcaccttttagtctatcccaggaagatgatcgctattacacagctatcaattttgaggc 3408

Query: 3552 tactcctgacgaacaaaacagggatttggacatgttcatcaatgcctccaagaatttcaa 3611
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 3409 tactcctgacgaacaaaacagggatttggacatgttcatcaatgcctccaagaatttcaa 3468

Query: 3612 cctcaacatcacctgggctgccagtttctcagctggaacccaggctggagaagagatgcc 3671
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 3469 cctcaacatcacctgggctgccagtttctcagctggaacccaggctggagaagagatgcc 3528

Query: 3672 tgttggtttcaaaaaccaacattaaggagtacaaagatagtttctctaagagaagtttga 3731
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 3529 tgttggtttcaaaaaccaacattaaggagtacaaagatagtttctctaagagaagtttga 3588

Query: 3732 ttttcgcaaccacccaaatatcactttctttgtttatgtcagtaatttcacctggcccat 3791
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 3589 ttttcgcaaccacccaaatatcactttctttgtttatgtcagtaatttcacctggcccat 3648

Query: 3792 caaaattcag 3801
 |||||||||
 Sbjct: 3649 caaaattcag 3658

Score = 182 bits (92), Expect = 4e-42
 Identities = 92/92 (100%)
 Strand = Plus / Plus

Query: 1 atgggtggctgcagcggcggaactgaggcaaggctgaggaggaggacggcggcgacggca 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 80 atgggtggctgcagcggcggaactgaggcaaggctgaggaggaggacggcggcgacggca 139

Query: 61 gcgctcgcgggcaggagcgggcgccgcactg 92
 ||||||||||||||||||||||||||||||||
 Sbjct: 140 gcgctcgcgggcaggagcgggcgccgcactg 171

Identity to membrane attractin (short 5' end)

100% identical base pairs over first 92 base pairs, then deleted region, then 100% identical over 3979 base pairs; therefore 100% identical over 92+3979 bp = 4071 bp, therefore 94.9% of reference length therefore 94.9% identical (?)

sequence not shown

Identity to kiaa0548/AB011120 coding region

Score = 2617 bits (1361), Expect = 0.0
 Identities = 1361/1361 (100%)
 Strand = Plus / Plus

100% identical 1361 base pairs but 31.73% of reference length therefore 31.73% identical.

Query: 3009 atacgatgagcacctgccccctgaaaattgttcaggctactgtacctgtagtcattgct 3068
 ||||||||||||||||||||||||||||||||||
 Sbjct: 1 atacgatgagcacctgccccctgaaaattgttcaggctactgtacctgtagtcattgct 60
 KIAA0548 protein 1 T M S T C P P E N C S G Y C T C S H C

Query: 3069 tggagcaaccaggctgtggctggtgtactgatcccagcaatactggcaaagggaaatgca 3128
 ||||||||||||||||||||||||||||||||||
 Sbjct: 61 tggagcaaccaggctgtggctggtgtactgatcccagcaatactggcaaagggaaatgca 120
 KIAA0548 protein 20 L E Q P G C G W C T D P S N T G K G K C

Query: 3129 tagagggttcctataaaggaccagtgaagatgccttcgcaagcccctacaggaaatttct 3188
 ||||||||||||||||||||||||||||||||||
 Sbjct: 121 tagagggttcctataaaggaccagtgaagatgccttcgcaagcccctacaggaaatttct 180
 KIAA0548 protein 40 I E G S Y K G P V K M P S Q A P T G N F

Query: 3189 atccacagcccctgctcaattccagcatgtgtctagaggacagcagatacaactggtctt 3248
 ||||||||||||||||||||||||||||||||||
 Sbjct: 181 atccacagcccctgctcaattccagcatgtgtctagaggacagcagatacaactggtctt 240
 KIAA0548 protein 60 Y P Q P L L N S S M C L E D S R Y N W S

Query: 3249 tcattcactgtccagcttgccaatgcaacggccacagtaaagcatcaatcagagcatct 3308
 ||||||||||||||||||||||||||||||||||
 Sbjct: 241 tcattcactgtccagcttgccaatgcaacggccacagtaaagcatcaatcagagcatct 300
 KIAA0548 protein 80 F I H C P A C Q C N G H S K C I N Q S I

Query: 3309 gtgagaagtgtgagaacctgaccacaggcaagcactgcgagacctgcataatctggtctt 3368
 ||||||||||||||||||||||||||||||||||
 Sbjct: 301 gtgagaagtgtgagaacctgaccacaggcaagcactgcgagacctgcataatctggtctt 360
 KIAA0548 protein 100 C E K C E N L T T G K H C E T C I S G F

Query: 3369 acggtgatcccaaatggagggaatgtcagccatgcaagtgcaatgggcacgcgtctc 3428

Sbjct: 361 |||
 KIAA0548 protein 120 Y G D P T N G G K C Q P C K C N G H A S 420

Query: 3429 tgtgcaacaccaacacgggcaagtgtctctgcaccaccaagggcggtcaagggggacgagt 3488
 Sbjct: 421 |||
 KIAA0548 protein 140 L C N T N T G K C F C T T K G V K G D E 480

Query: 3489 gccagctatgtgaggtagaaaatcgataccaaggaaaccctctcagaggaacatgttatt 3548
 Sbjct: 481 |||
 KIAA0548 protein 160 C Q L C E V E N R Y Q G N P L R G T C Y 540

Query: 3549 atactcttcttattgactatcagttcaccttttagtctatcccaggaagatgatcgctatt 3608
 Sbjct: 541 |||
 KIAA0548 protein 180 Y T L L I D Y Q F T F S L S Q E D D R Y 600

Query: 3609 acacagctatcaatthttgtggctactcctgacgaacaaaacagggtttggacatgttca 3668
 Sbjct: 601 |||
 KIAA0548 protein 200 Y T A I N F V A T P D E Q N R D L D M F 660

Query: 3669 tcaatgcctccaagaatttcaacctcaacatcacctgggctgccagtttctcagctggaa 3728
 Sbjct: 661 |||
 KIAA0548 protein 220 I N A S K N F N L N I T W A A S F S A G 720

Query: 3729 cccaggctggagaagagatgcctgttgtttcaaaaaccaacattaaggagtacaaagata 3788
 Sbjct: 721 |||
 KIAA0548 protein 240 T Q A G E E M P V V S K T N I K E Y K D 780

Query: 3789 gtttctctaagtgaagtttgattttcgcaaccacccaaatatcactttctttgtttatg 3848
 Sbjct: 781 |||
 KIAA0548 protein 260 S F S N E K F D F R N H P N I T F F V Y 840

Query: 3849 tcagtaatttcacctggcccatcaaaattcagattgccttctctcagcacagcaatttta 3908
 Sbjct: 841 |||
 KIAA0548 protein 280 V S N F T W P I K I Q I A F S Q H S N F 900

Query: 3909 tggacctggtacagttcttcgtgactttcttcagttgtttcctctctttgctcctggtgg 3968
 Sbjct: 901 |||
 KIAA0548 protein 300 M D L V Q F F V T F F S C F L S L L L V 960

Query: 3969 ctgctgtggttttgaagatcaaacaaagtgttgggcctccagacgtagagagcaacttc 4028
 Sbjct: 961 |||
 KIAA0548 protein 320 A A V V W K I K Q S C W A S R R R E Q L 1020

Query: 4029 ttcgagagatgcaacagatggccagccgtccctttgcctctgtaaagtgcgccttgga 4088
 ||||||||||||||||||
 Sbjct: 1021 ttcgagagatgcaacagatggccagccgtccctttgcctctgtaaagtgcgccttgga 1080
 KIAA0548 protein 340 L R E M Q Q M A S R P F A S V N V A L E

Query: 4089 cagatgaggagcctcctgatcttattggggggagtataaagactgttcccaaaccattg 4148
 ||||||||||||||||||
 Sbjct: 1081 cagatgaggagcctcctgatcttattggggggagtataaagactgttcccaaaccattg 1140
 KIAA0548 protein 360 T D E E P P D L I G G S I K T V P K P I

Query: 4149 cactggagccgtgttttggcaacaaagccgctgtcctctctgtgtttgtgaggctccctc 4208
 ||||||||||||||||||
 Sbjct: 1141 cactggagccgtgttttggcaacaaagccgctgtcctctctgtgtttgtgaggctccctc 1200
 KIAA0548 protein 380 A L E P C F G N K A A V L S V F V R L P

Query: 4209 gaggcctgggtggcatccctcctcctgggcagtcaggtcttgctgtggccagcgccttg 4268
 ||||||||||||||||||
 Sbjct: 1201 gaggcctgggtggcatccctcctcctgggcagtcaggtcttgctgtggccagcgccttg 1260
 KIAA0548 protein 400 R G L G G I P P P G Q S G L A V A S A L

Query: 4269 tggacatttctcagcagatgccgatagtgtacaaggagaagtcaggagccgtgagaaacc 4328
 ||||||||||||||||||
 Sbjct: 1261 tggacatttctcagcagatgccgatagtgtacaaggagaagtcaggagccgtgagaaacc 1320
 KIAA0548 protein 420 V D I S Q Q M P I V Y K E K S G A V R N

Query: 4329 ggaagcagcagccccctgcacagcctgggacctgcatctga 4369
 ||||||||||||||||||
 Sbjct: 1321 ggaagcagcagccccctgcacagcctgggacctgcatctga 1361
 KIAA0548 protein 440 R K Q Q P P A Q P G T C I ^^^